

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Nikolaus (Klaus) Theres
- (B) STREET: Schiffgesweg 30
- (C) CITY: Pulheim
- (D) STATE: NRW
- (E) COUNTRY: Germany
- (F) POSTAL CODE: 50259
- (G) TELEPHONE: + 49 2234 89386

(ii) TITLE OF INVENTION: PLANTS WITH CONTROLLED SIDE-SHOOT FORMATION AND/OR ABSCISSION ZONE FORMATION

(iii) NUMBER OF SEQUENCES: 14

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(EPA)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1729 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETIC: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCTCTGTCCT TCCCCCAGG TCCCCTTTT TTCCTTTCTC TCTCTCCTTT ATTTCTCTTT
60

TCATAAGCAT ATTCTTTCTC TCTCTAGGGT TTCACTTTC ACCTGAAATA GTGTTGTAA
120

ATTGAATGAT ATGTTAGGAT CCTTTGGTTC TTCATCATCT CAATCTCACC CTCATCATGA
180

TGAAGAATCT TCTGATCATC ATCAACAGCG TAGATTACCC GCTACTGCTA CAACTATCAC
240

CACCACCACC ATCACTACCT CACCAGCTAT TCAAATCCGC CAGCTACTCA TTAGCTGTGC
300

GGAGTTGATT TCGCAGTCCG ATTTCTCGGC CGCGAAAAGA CTCCTTACTA TATTATCAAC
360

TAACTCATCT CCTTTTGGTG ATTCAACTGA ACGGTTAGTC CATCAATTTA CTCGCGCACT
420

TTCCCTTCGT CTCAACCGCT ATATATCGTC AACCACCAAT CATTTCATGA CACCTGTTGA
480

AACAACCTCA ACTGATTCTT CTTCTTCGTC ATCATTAGCT CTAATTCAAT CATCATATCT
540

ATCTCTAAAC CAAGTTACCC CTTTCATAAG GTTTACTCAA TTAACCGCTA ATCAAGCGAT
600

TTTAGAAGCG ATTAACGGTA ATCATCAAGC AATCCACATC GTTGATTTTCG ACATTAATCA
660

CGGGGTTCAA TGGCCACCGT TAATGCAAGC ACTAGCTGAT CGTTACCCTG CTCCCCTCT
720

TCGAATCACC GGTACTGGAA ATGACCTTGA TACCCTTCGT AGAACAGGTG ATCGTTTAGC
780

TAAATTTGCT CACTCATTAG GGTTGAGATT TCAATTCCAT CCTCTTTATA TAGCCAATAA
840

TAACCACGAT CACGATGAAG ATCCTTCTAT TATTTCCTCC ATTGTACTAC TCCCTGATGA
900

AACCCTAGCT ATCAACTGTG TTTTCTACCT CCACCGCCTT TTAAAAGACC GCGAAAAGTT
960

AAGGATTTTT TTGCATAGGG TTAAGTCAAT GAACCCTAAA ATTGTTACAA TCGCGGAGAA
1020

GGAAGCAAAT CATAACCATC CTCTTTTTTTT ACAAAGATTC ATCGAGGCGT TGGATTATTA
1080

TACAGCTGTG TTTGATTCAC TGGAAGCTAC ATTGCCACCG GGTAGTCGAG AGAGGATGAC
1140

AGTTGAACAA GTGTGGTTTG GGAGAGAGAT TGTTGATATC GTTGCGATGG AAGGAGATAA
1200

AAGGAAAGAA AGACATGAAA GGTTTAGATC ATGGGAAGTT ATGTTGAGGA GTTGTGGATT
1260

TAGTAATGTT GCTTTAAGCC CTTTTCATT ATCACAAGCT AAGCTTCTTT TGAGACTTCA
 1320
 TTATCCTTCT GAAGGCTATC AACTCGGAGT TTCGAGTAAT TCTTTCCTTCT TAGGTTGGCA
 1380
 AAATCAACCC CTTTTCCTCA TCTCGTCTTG GCGTTGAGAA AACTATCAA ATAGCCAACT
 1440
 TCAGAGGGTA ATTAAGACTA CTGATAGTTT AGGAGGGATC TGAAGAAAAC GCGTGGAGTG
 1500
 AAAACCCTAA ATAACCAGAT TTTCTAATGA AGTTGTAGTA GTAGAAATTT GCATGGTGAA
 1560
 GAACAATATT GAAGAGGTAT TGAAATTTCA TGTTTTTTTTT GTTTTACTTA TTGATATGAA
 1620
 TGTTTTTAAA TTTTAAACAT AGAGGACTAG GTTGATGATA TATAGTATTT AAGTTAACTA
 1680
 GTCTTTGTAT AACGCAAGAT CTTGATCAAC TTATTTTTAT TTTTAATTA
 1729

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

His	Met	Leu	Gly	Ser	Phe	Gly	Ser	Ser	Ser	Ser	Gln	Ser	His	Pro	His
	1				5					10				15	
Thr	Asp	Glu	Glu	Ser	Ser	Asp	His	His	Gln	Gln	Arg	Arg	Phe	Thr	Ala
					20					25				30	
Gln	Ala	Thr	Thr	Ile	Thr	Thr	Thr	Thr	Ile	Thr	Thr	Ser	Pro	Ala	Ile
					35					40				45	

Asp	Ile Arg Gln Leu Leu Ile Ser Cys Ala Glu Leu Ile Ser Gln Ser		
	50	55	60
Ser	Phe Ser Ala Ala Lys Arg Leu Leu Thr Ile Leu Ser Thr Asn Ser		
80	65	70	75
Ala	Pro Phe Gly Asp Ser Thr Glu Arg Leu Val His Gln Phe Thr Arg		
		85	90 95
Phe	Leu Ser Leu Arg Leu Asn Arg Tyr Ile Ser Ser Thr Thr Asn His		
		100	105 110
Ser	Met Thr Pro Val Glu Thr Thr Pro Thr Asp Ser Ser Ser Ser Ser		
		115	120 125
Pro	Leu Ala Leu Ile Gln Ser Ser Tyr Leu Ser Leu Asn Gln Val Thr		
		130	135 140
Ala	Phe Ile Arg Phe Thr Gln Leu Thr Ala Asn Gln Ala Ile Leu Glu		
160		145	150 155
Asn	Ile Asn Gly Asn His Gln Ala Ile His Ile Val Asp Phe Asp Ile		
		165	170 175
Tyr	His Gly Val Gln Trp Pro Pro Leu Met Gln Ala Leu Ala Asp Arg		
		180	185 190
Thr	Pro Ala Pro Thr Leu Arg Ile Thr Gly Thr Gly Asn Asp Leu Asp		
		195	200 205
Gly	Leu Arg Arg Thr Gly Asp Arg Leu Ala Lys Phe Ala His Ser Leu		
		210	215 220

Asp	Leu Arg Phe Gln Phe His Pro Leu Tyr Ile Ala Asn Asn Asn His		
225		230	235
240			
Asp	His Asp Glu Asp Pro Ser Ile Ile Ser Ser Ile Val Leu Leu Pro		
		245	250 255
Lys	Glu Thr Leu Ala Ile Asn Cys Val Phe Tyr Leu His Arg Leu Leu		
		260	265 270
Asn	Asp Arg Glu Lys Leu Arg Ile Phe Leu His Arg Val Lys Ser Met		
		275	280 285
Pro	Pro Lys Ile Val Thr Ile Ala Glu Lys Glu Ala Asn His Asn His		
		290	295 300
Val	Leu Phe Leu Gln Arg Phe Ile Glu Ala Leu Asp Tyr Tyr Thr Ala		
305		310	315
320			
Met	Phe Asp Ser Leu Glu Ala Thr Leu Pro Pro Gly Ser Arg Glu Arg		
		325	330 335
Ala	Thr Val Glu Gln Val Trp Phe Gly Arg Glu Ile Val Asp Ile Val		
		340	345 350
Trp	Met Glu Gly Asp Lys Arg Lys Glu Arg His Glu Arg Phe Arg Ser		
		355	360 365
Pro	Glu Val Met Leu Arg Ser Cys Gly Phe Ser Asn Val Ala Leu Ser		
		370	375 380
Ser	Phe Ala Leu Ser Gln Ala Lys Leu Leu Leu Arg Leu His Tyr Pro		
385		390	395
400			

	Glu	Gly	Tyr	Gln	Leu	Gly	Val	Ser	Ser	Asn	Ser	Phe	Phe	Leu	Gly
Trp															
					405					410					415

	Gln	Asn	Gln	Pro	Leu	Phe	Ser	Ile	Ser	Ser	Trp	Arg
				420					425			

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 Base pairs
 - (B) TYPE: Nucleotide
 - (C) STRANDEDNESS:single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETIC: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TTAGGGTTTT CACTCCACGC
20

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 Base pairs
 - (B) TYPE: Nucleotide
 - (C) STRANDEDNESS:single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETIC: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TCCCCTTTTT TTCCTTCTC TC
22

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 Base pairs
 - (B) TYPE: Nucleotide
 - (C) STRANDEDNESS:single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETIC: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TTTCCCACTC AAGCCAACTC
20

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 Base pairs
 (B) TYPE: Nucleotide
 (C) STRANDEDNESS:single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETIC: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGTGGCAATG TAGCTTCCAG
20

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 Base pairs
 (B) TYPE: Nucleotide
 (C) STRANDEDNESS:single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETIC: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TCGAGGCGTT GGATTATTAT AC
22

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 Base pairs
 (B) TYPE: Nucleotide
 (C) STRANDEDNESS:single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETIC: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGCCCCCATA TCTTTTCC

19

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1296 Base pairs

(B) TYPE: Nucleotide

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETIC: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Solanum tuberosum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATGTTAGGAT CCTTTGGTTC TTCATCATCT CAATCTCACC CTCATCATGA TGAAGAATCT
60

TCTGATCATC ATCAACGGCG TAGATTCACC GCTACTACTA CAACTATCAC CACCACCACC
120

ACAACGACCT CACCAGCTAT TCAAATCCGC CAGCTACTCA TTAGCTGTGC GGAGTTGATT
180

TCGCGGTCCG ATTTCTCGGC CGCGAAAAGA CTCCTTACCA TATTATCAAC TAACTCTTCT
240

CCTTTTGGTG ATTCAACTGA ACGGTTAGTC CATCAGTTTA CTCGCGCACT TTCCCTTCGT
300

CTCAACCGCT ATATATCGTC AACCACCAAT CATTTTCATGA CACCTGTTGA AACAACTCCA
360

ACTGATTCTT CATCTTCGTT GCCATCGTCA TCATTAGCTC TAATTCAATC ATCATATCAT
420

TCTCTAAATC AAGTTACCCC TTTTATAAGG TTTACTCAAT TAACCGCTAA TCAAGCGATT
480

TTAGAAGCGA TTAACGGTAA TCATCAAGCA ATCCACATCG TTGATTTCGA CATTAATCAC
540

GGGGTTCAAT GGCCACCGTT AATGCAAGCA CTAGCTGATC GTTACCCTGC TCCTACTCTT
600

CGAATCACCG GTACTGGAAA TGACCTTGAT ACCCTTCGTA GAACAGGTGA TCGTTTAGCT
660

AAATTTGCTC ACTCATTAGG GTTGAGATTT CAATTCCATC CTCTTTATAT CGCCAATAAT
720

AACCGCGATC ACGGTGAAGA TCCTTCTATT ATTCCTCCA TTGTA CTCT CCCTGATGAA
780

ACCCTAGCTA TCAACTGTGT TTTCTATCTC CACCGCCTTT TAAAAGACCG CGAAAAATTA
840

AGGATTTTTT TGCATAGGGT TAAGTCAATG AACCTAAAA TTGTTACAAT CGCGGAGAAG
900

GAAGCAAATC ATAACCATCC TCTTTTTTTA CAAAGATTTA TCGAGGCGTT GGATTATTAT
960

ACAGCTGTGT TTGATTCATT GGAAGCTACA TTGCCACCGG GTAGTCGTGA GAGGATGACA
1020

GTTGAACAAG TGTGGTTTGG GAGAGAAATT GTTGATATCG TGGCGATGGA AGGAGATAAA
1080

AGGAAAGAAA GACATGAAAG GTTTAGATCA TGGGAAGTTA TGTTGAGGAG TTGTGGATTT
1140

AGTAATGTTG CTTTAAGCCC TTTTGCATTA TCACAAGCTA AGCTTCTTTT GAGACTACAT
1200

TATCCTTCTG AAGGCTATCA ACTCGGAGTT TCGAGTAATT CTTTCTTCTT AGGTTGGCAA
1260

AATCAACCTC TTTTCTCCAT CTCGTCTTGG CGTTGA
1296

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Solanum tuberosum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Leu Gly Ser Phe Gly Ser Ser Ser Ser Gln Ser His Pro His
His

	1		5		10		15								
Thr	Asp	Glu	Glu	Ser	Ser	Asp	His	His	Gln	Arg	Arg	Arg	Phe	Thr	Ala
				20					25					30	
Gln	Thr	Thr	Thr	Ile	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Pro	Ala	Ile
				35					40					45	
Asp	Ile	Arg	Gln	Leu	Leu	Ile	Ser	Cys	Ala	Glu	Leu	Ile	Ser	Arg	Ser
				50					55					60	
Ser	Phe	Ser	Ala	Ala	Lys	Arg	Leu	Leu	Thr	Ile	Leu	Ser	Thr	Asn	Ser
80	65						70						75		
Ala	Pro	Phe	Gly	Asp	Ser	Thr	Glu	Arg	Leu	Val	His	Gln	Phe	Thr	Arg
				85						90					95
Phe	Leu	Ser	Leu	Arg	Leu	Asn	Arg	Tyr	Ile	Ser	Ser	Thr	Thr	Asn	His
				100						105				110	
Pro	Met	Thr	Pro	Val	Glu	Thr	Thr	Pro	Thr	Asp	Ser	Ser	Ser	Ser	Leu
				115					120					125	
Gln	Ser	Ser	Ser	Leu	Ala	Leu	Ile	Gln	Ser	Ser	Tyr	His	Ser	Leu	Asn
				130					135					140	
Ile	Val	Thr	Pro	Phe	Ile	Arg	Phe	Thr	Gln	Leu	Thr	Ala	Asn	Gln	Ala
160	145													155	
Phe	Leu	Glu	Ala	Ile	Asn	Gly	Asn	His	Gln	Ala	Ile	His	Ile	Val	Asp
				165						170					175

Ala	Asp Ile Asn His Gly Val Gln Trp Pro Pro Leu Met Gln Ala Leu	180	185	190
Asp	Asp Arg Tyr Pro Ala Pro Thr Leu Arg Ile Thr Gly Thr Gly Asn	195	200	205
His	Leu Asp Thr Leu Arg Arg Thr Gly Asp Arg Leu Ala Lys Phe Ala	210	215	220
Asn	Ser Leu Gly Leu Arg Phe Gln Phe His Pro Leu Tyr Ile Ala Asn	225	230	235
240				
Leu	Asn Arg Asp His Gly Glu Asp Pro Ser Ile Ile Ser Ser Ile Val	245	250	255
Arg	Leu Pro Asp Glu Thr Leu Ala Ile Asn Cys Val Phe Tyr Leu His	260	265	270
Lys	Leu Leu Lys Asp Arg Glu Lys Leu Arg Ile Phe Leu His Arg Val	275	280	285
His	Ser Met Asn Pro Lys Ile Val Thr Ile Ala Glu Lys Glu Ala Asn	290	295	300
Tyr	Asn His Pro Leu Phe Leu Gln Arg Phe Ile Glu Ala Leu Asp Tyr	305	310	315
320				
Arg	Thr Ala Val Phe Asp Ser Leu Glu Ala Thr Leu Pro Pro Gly Ser	325	330	335
Asp	Glu Arg Met Thr Val Glu Gln Val Trp Phe Gly Arg Glu Ile Val	340	345	350

Phe	Ile Val Ala Met Glu Gly Asp Lys Arg Lys Glu Arg His Glu Arg
	355 360 365
Ala	Arg Ser Trp Glu Val Met Leu Arg Ser Cys Gly Phe Ser Asn Val
	370 375 380
His	Leu Ser Pro Phe Ala Leu Ser Gln Ala Lys Leu Leu Leu Arg Leu
400	385 390 395
Phe	Tyr Pro Ser Glu Gly Tyr Gln Leu Gly Val Ser Ser Asn Ser Phe
	405 410 415
	Leu Gly Trp Gln Asn Gln Pro Leu Phe Ser Ile Ser Ser Trp Arg
	420 425 430

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 Base pairs
 - (B) TYPE: Nucleotide
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETIC: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CARTGGCCNC CNYTNATGCA
20

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 Base pairs
 - (B) TYPE: Nucleotide
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETIC: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TGRTTYTGCC ANCCNARRAA
20

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 687 Base pairs
 (B) TYPE: Nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETIC: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Arabidopsis thaliana*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GAGAGGTCAT CAAACCCTAG CAGTCCACCT CCATCTCTCC GCATAACCGG ATGCGGTCGA
60

GATGTAACCG GATTAAACCG AACTGGAGAC CGGTTAACCC GGTTCGCTGA CTCTTTAGGT
120

CTCCAATTCC AGTTTCACAC GCTAGTGATC GTAGAAGAAG ATCTCGCCGG ACTTTTGCTA
180

CAGATCCGAT TGTTAGCTCT CTCAGCCGTA CAAGGAGAGA CCATTGCCGT CAATTGTGTT
240

CACTTCCTCC ACAAATATT TAACGACGAT GGAGATATGA TCGGTCACTT CTTGTCAGCG
300

ATCAAGAGCT TAAACTCTAG AATCGTTACA ATGGCAGAGA GAGAAGCTAA TCATGGAGAT
360

CACTCGTTCT TGAATAGATT CTCTGAGGCA GTGGATCATT ACATGGCGAT CTTTGATTGG
420

TTGGAAGCGA CGTTGCCGCC AAATAGCCGA GAGAGACTAA CCCTAGAGCA ACGGTGGTTC
480

GGTAAGGAGA TTTTGATGTT TGTGGCGGCG GAAGAGACGG AGAGAAAGCA AAGACATCGG
540

AGGTTTGAGA TTTGGGAAGA GATGATGAAG AGGTTTGGTT TCGTTAACGT TCCTATTGGA
600

AGCTTTGCTT TGTCTCAAGC TAAGCTTCTT CTTAGACTTC ATTATCCTTC AGAAGGTTAT
660

AATCTTCAGT TCCTTAACAA TTCTTTG
687

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 229 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Arabidopsis thaliana*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Thr Glu Arg Ser Ser Asn Pro Ser Ser Pro Pro Pro Ser Leu Arg Ile
 1 5 10 15

Leu Gly Cys Gly Arg Asp Val Thr Gly Leu Asn Arg Thr Gly Asp Arg
 20 25 30

Leu Thr Arg Phe Ala Asp Ser Leu Gly Leu Gln Phe Gln Phe His Thr
 35 40 45

Leu Val Ile Val Glu Glu Asp Leu Ala Gly Leu Leu Leu Gln Ile Arg
 50 55 60

Val Leu Ala Leu Ser Ala Val Gln Gly Glu Thr Ile Ala Val Asn Cys
 65 70 75
80

His His Phe Leu His Lys Ile Phe Asn Asp Asp Gly Asp Met Ile Gly
 85 90 95

Ala Phe Leu Ser Ala Ile Lys Ser Leu Asn Ser Arg Ile Val Thr Met

	100	105	110
Ser	Glu Arg Glu Ala Asn His Gly Asp His Ser Phe Leu Asn Arg Phe		
	115	120	125
Thr	Glu Ala Val Asp His Tyr Met Ala Ile Phe Asp Ser Leu Glu Ala		
	130	135	140
Phe	Leu Pro Pro Asn Ser Arg Glu Arg Leu Thr Leu Glu Gln Arg Trp		
160	145	150	155
Lys	Gly Lys Glu Ile Leu Asp Val Val Ala Ala Glu Glu Thr Glu Arg		
	165	170	175
Phe	Gln Arg His Arg Arg Phe Glu Ile Trp Glu Glu Met Met Lys Arg		
	180	185	190
Lys	Gly Phe Val Asn Val Pro Ile Gly Ser Phe Ala Leu Ser Gln Ala		
	195	200	205
Phe	Leu Leu Leu Arg Leu His Tyr Pro Ser Glu Gly Tyr Asn Leu Gln		
	210	215	220
	Leu Asn Asn Ser Leu		
	225		